

RAW SEQUENCE LISTING

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Application Serial Number: 10/568,578
Source: IFWP
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IFWP

RAW SEQUENCE LISTING

DATE: 02/01/2007

PATENT APPLICATION: US/10/568,578

TIME: 12:16:16

Input Set : A:\02856701.APP

Output Set: N:\CRF4\02012007\J568578.raw

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3 <110> APPLICANT: HIHARA, SATOSHI
4     DOI, HIROFUMI
6 <120> TITLE OF INVENTION: INTERACTION INHIBITORS, METHOD OF DETECTING INTERACTION
7     INHIBITOR AND KIT FOR DETECTING INTERACTION INHIBITOR
9 <130> FILE REFERENCE: 028567-0145
11 <140> CURRENT APPLICATION NUMBER: 10/568,578
12 <141> CURRENT FILING DATE: 2006-02-17
14 <150> PRIOR APPLICATION NUMBER: PCT/JP2004/011686
15 <151> PRIOR FILING DATE: 2004-08-13
17 <150> PRIOR APPLICATION NUMBER: JP 2003-295204
18 <151> PRIOR FILING DATE: 2003-08-19
20 <160> NUMBER OF SEQ ID NOS: 11
22 <170> SOFTWARE: PatentIn Ver. 3.3
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 23
26 <212> TYPE: DNA
27 <213> ORGANISM: Artificial Sequence
29 <220> FEATURE:
30 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
31     primer
33 <400> SEQUENCE: 1
34 atgtcgccat ttcttcggat tgg                                     23
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38 <211> LENGTH: 19
39 <212> TYPE: DNA
40 <213> ORGANISM: Artificial Sequence
42 <220> FEATURE:
43 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
44     primer
46 <400> SEQUENCE: 2
47 tcaggatatc agccgctcc                                         19
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51 <211> LENGTH: 21
52 <212> TYPE: DNA
53 <213> ORGANISM: Artificial Sequence
55 <220> FEATURE:
56 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
57     primer
59 <400> SEQUENCE: 3
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63 <210> SEQ ID NO: 4
64 <211> LENGTH: 19
65 <212> TYPE: DNA

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66 <213> ORGANISM: Artificial Sequence
68 <220> FEATURE:
69 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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77 <211> LENGTH: 35
78 <212> TYPE: DNA
79 <213> ORGANISM: Artificial Sequence
81 <220> FEATURE:
82 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
83     primer
85 <400> SEQUENCE: 5
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89 <210> SEQ ID NO: 6
90 <211> LENGTH: 30
91 <212> TYPE: DNA
92 <213> ORGANISM: Artificial Sequence
94 <220> FEATURE:
95 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
96     primer
98 <400> SEQUENCE: 6
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103 <211> LENGTH: 30
104 <212> TYPE: DNA
105 <213> ORGANISM: Artificial Sequence
107 <220> FEATURE:
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120 <220> FEATURE:
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129 <211> LENGTH: 706
130 <212> TYPE: PRT
131 <213> ORGANISM: Homo sapiens
133 <400> SEQUENCE: 9
134 Met Ser Pro Phe Leu Arg Ile Gly Leu Ser Asn Phe Asp Cys Gly Ser
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137 Cys Gln Ser Cys Gln Gly Glu Ala Val Asn Pro Tyr Cys Ala Val Leu
138          20          25          30
140 Val Lys Glu Tyr Val Glu Ser Glu Asn Gly Gln Met Tyr Ile Gln Lys
141          35          40          45
143 Lys Pro Thr Met Tyr Pro Pro Trp Asp Ser Thr Phe Asp Ala His Ile
144          50          55          60
146 Asn Lys Gly Arg Val Met Gln Ile Ile Val Lys Gly Lys Asn Val Asp
147 65          70          75          80
149 Leu Ile Ser Glu Thr Thr Val Glu Leu Tyr Ser Leu Ala Glu Arg Cys
150          85          90          95
152 Arg Lys Asn Asn Gly Lys Thr Glu Ile Trp Leu Glu Leu Lys Pro Gln
153          100          105          110
155 Gly Arg Met Leu Met Asn Ala Arg Tyr Phe Leu Glu Met Ser Asp Thr
156          115          120          125
158 Lys Asp Met Asn Glu Phe Glu Thr Glu Gly Phe Phe Ala Leu His Gln
159          130          135          140
161 Arg Arg Gly Glu Ile Lys Gln Ala Lys Val His His Val Lys Cys His
162 145          150          155          160
164 Glu Phe Thr Ala Thr Phe Phe Pro Gln Pro Thr Phe Cys Ser Val Cys
165          165          170          175
167 His Glu Phe Val Trp Gly Leu Asn Lys Gln Gly Tyr Gln Cys Arg Gln
168          180          185          190
170 Cys Asn Ala Ala Ile His Lys Lys Cys Ile Asp Lys Val Ile Ala Lys
171          195          200          205
173 Cys Thr Gly Ser Ala Ile Asn Ser Arg Glu Thr Met Phe His Lys Glu
174          210          215          220
176 Arg Phe Lys Ile Asp Met Pro His Arg Phe Lys Val Tyr Asn Tyr Lys
177 225          230          235          240
179 Ser Pro Thr Phe Cys Glu His Cys Gly Thr Leu Leu Trp Gly Leu Ala
180          245          250          255
182 Arg Gln Gly Leu Lys Cys Asp Ala Cys Gly Met Asn Val His His Arg
183          260          265          270
185 Cys Gln Thr Lys Val Ala Asn Leu Cys Gly Ile Asn Gln Lys Leu Met
186          275          280          285
188 Ala Glu Ala Leu Ala Met Ile Glu Ser Thr Gln Gln Ala Arg Cys Leu
189          290          295          300
191 Arg Asp Thr Glu Gln Ile Phe Arg Glu Gly Pro Val Glu Ile Gly Leu
192 305          310          315          320
194 Pro Cys Ser Ile Lys Asn Glu Ala Arg Pro Pro Cys Leu Pro Thr Pro
195          325          330          335
197 Gly Lys Arg Glu Pro Gln Gly Ile Ser Trp Glu Ser Pro Leu Asp Glu
198          340          345          350
200 Val Asp Lys Met Cys His Leu Pro Glu Pro Glu Leu Asn Lys Glu Arg
201          355          360          365
203 Pro Ser Leu Gln Ile Lys Leu Lys Ile Glu Asp Phe Ile Leu His Lys
204          370          375          380
206 Met Leu Gly Lys Gly Ser Phe Gly Lys Val Phe Leu Ala Glu Phe Lys
207 385          390          395          400
209 Lys Thr Asn Gln Phe Phe Ala Ile Lys Ala Leu Lys Lys Asp Val Val

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210          405          410          415
212 Leu Met Asp Asp Asp Val Glu Cys Thr Met Val Glu Lys Arg Val Leu
213          420          425          430
215 Ser Leu Ala Trp Glu His Pro Phe Leu Thr His Met Phe Cys Thr Phe
216          435          440          445
218 Gln Thr Lys Glu Asn Leu Phe Phe Val Met Glu Tyr Leu Asn Gly Gly
219          450          455          460
221 Asp Leu Met Tyr His Ile Gln Ser Cys His Lys Phe Asp Leu Ser Arg
222 465          470          475          480
224 Ala Thr Phe Tyr Ala Ala Glu Ile Ile Leu Gly Leu Gln Phe Leu His
225          485          490          495
227 Ser Lys Gly Ile Val Tyr Arg Asp Leu Lys Leu Asp Asn Ile Leu Leu
228          500          505          510
230 Asp Lys Asp Gly His Ile Lys Ile Ala Asp Phe Gly Met Cys Lys Glu
231          515          520          525
233 Asn Met Leu Gly Asp Ala Lys Thr Asn Thr Phe Cys Gly Thr Pro Asp
234          530          535          540
236 Tyr Ile Ala Pro Glu Ile Leu Leu Gly Gln Lys Tyr Asn His Ser Val
237 545          550          555          560
239 Asp Trp Trp Ser Phe Gly Val Leu Leu Tyr Glu Met Leu Ile Gly Gln
240          565          570          575
242 Ser Pro Phe His Gly Gln Asp Glu Glu Glu Leu Phe His Ser Ile Arg
243          580          585          590
245 Met Asp Asn Pro Phe Tyr Pro Arg Trp Leu Glu Lys Glu Ala Lys Asp
246          595          600          605
248 Leu Leu Val Lys Leu Phe Val Arg Glu Pro Glu Lys Arg Leu Gly Val
249          610          615          620
251 Arg Gly Asp Ile Arg Gln His Pro Leu Phe Arg Glu Ile Asn Trp Glu
252 625          630          635          640
254 Glu Leu Glu Arg Lys Glu Ile Asp Pro Pro Phe Arg Pro Lys Val Lys
255          645          650          655
257 Ser Pro Phe Asp Cys Ser Asn Phe Asp Lys Glu Phe Leu Asn Glu Lys
258          660          665          670
260 Pro Arg Leu Ser Phe Ala Asp Arg Ala Leu Ile Asn Ser Met Asp Gln
261          675          680          685
263 Asn Met Phe Arg Asn Phe Ser Phe Met Asn Pro Gly Met Glu Arg Leu
264          690          695          700
266 Ile Ser
267 705
270 <210> SEQ ID NO: 10
271 <211> LENGTH: 706
272 <212> TYPE: PRT
273 <213> ORGANISM: Homo sapiens
275 <400> SEQUENCE: 10
276 Met Ser Pro Phe Leu Arg Ile Gly Leu Ser Asn Phe Asp Cys Gly Ser
277 1 5 10 15
279 Cys Gln Ser Cys Gln Gly Glu Ala Val Asn Pro Tyr Cys Ala Val Leu
280 20 25 30
282 Val Lys Glu Tyr Val Glu Ser Glu Asn Gly Gln Met Tyr Ile Gln Lys

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283          35          40          45
285 Lys Pro Thr Met Tyr Pro Pro Trp Asp Ser Thr Phe Asp Ala His Ile
286          50          55          60
288 Asn Lys Gly Arg Val Met Gln Ile Ile Val Lys Gly Lys Asn Val Asp
289 65          70          75          80
291 Leu Ile Ser Glu Thr Thr Val Glu Leu Tyr Ser Leu Ala Glu Arg Cys
292          85          90          95
294 Arg Lys Asn Asn Gly Lys Thr Glu Ile Trp Leu Glu Leu Lys Pro Gln
295          100          105          110
297 Gly Arg Met Leu Met Asn Ala Arg Tyr Phe Leu Glu Met Ser Asp Thr
298          115          120          125
300 Lys Asp Met Asn Glu Phe Glu Thr Glu Gly Phe Phe Ala Leu His Gln
301          130          135          140
303 Arg Arg Gly Ala Ile Lys Gln Ala Lys Val His His Val Lys Cys His
304 145          150          155          160
306 Glu Phe Thr Ala Thr Phe Phe Pro Gln Pro Thr Phe Cys Ser Val Cys
307          165          170          175
309 His Glu Phe Val Trp Gly Leu Asn Lys Gln Gly Tyr Gln Cys Arg Gln
310          180          185          190
312 Cys Asn Ala Ala Ile His Lys Lys Cys Ile Asp Lys Val Ile Ala Lys
313          195          200          205
315 Cys Thr Gly Ser Ala Ile Asn Ser Arg Glu Thr Met Phe His Lys Glu
316          210          215          220
318 Arg Phe Lys Ile Asp Met Pro His Arg Phe Lys Val Tyr Asn Tyr Lys
319 225          230          235          240
321 Ser Pro Thr Phe Cys Glu His Cys Gly Thr Leu Leu Trp Gly Leu Ala
322          245          250          255
324 Arg Gln Gly Leu Lys Cys Asp Ala Cys Gly Met Asn Val His His Arg
325          260          265          270
327 Cys Gln Thr Lys Val Ala Asn Leu Cys Gly Ile Asn Gln Lys Leu Met
328          275          280          285
330 Ala Glu Ala Leu Ala Met Ile Glu Ser Thr Gln Gln Ala Arg Cys Leu
331          290          295          300
333 Arg Asp Thr Glu Gln Ile Phe Arg Glu Gly Pro Val Glu Ile Gly Leu
334 305          310          315          320
336 Pro Cys Ser Ile Lys Asn Glu Ala Arg Pro Pro Cys Leu Pro Thr Pro
337          325          330          335
339 Gly Lys Arg Glu Pro Gln Gly Ile Ser Trp Glu Ser Pro Leu Asp Glu
340          340          345          350
342 Val Asp Lys Met Cys His Leu Pro Glu Pro Glu Leu Asn Lys Glu Arg
343          355          360          365
345 Pro Ser Leu Gln Ile Lys Leu Lys Ile Glu Asp Phe Ile Leu His Lys
346          370          375          380
348 Met Leu Gly Lys Gly Ser Phe Gly Lys Val Phe Leu Ala Glu Phe Lys
349 385          390          395          400
351 Lys Thr Asn Gln Phe Phe Ala Ile Arg Ala Leu Lys Lys Asp Val Val
352          405          410          415
354 Leu Met Asp Asp Asp Val Glu Cys Thr Met Val Glu Lys Arg Val Leu
355          420          425          430

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